

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 11:09:29 ; Search time 13.2396 Seconds
(without alignments)
6706.854 Million cell updates/sec

Title: US-10-750-965-40

Perfect score: 15

Sequence: 1 gaacagatctgga 15

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: N_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
- 6: Geneseq2002as:*
- 7: Geneseq2002bs:*
- 8: Geneseq2003as:*
- 9: Geneseq2003bs:*
- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004as:*
- 13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	AAA07571	AAA07571 Detoxifile
2	15	100.0	322	AD171247	AD171247 Human ova
3	15	100.0	322	AD136407	AD136407 Human ova
4	15	100.0	385	AD142791	AD142791 Human ova
5	15	100.0	556	AD142842	AD142842 Human ova
6	15	100.0	672	AAK84821	AAK84821 Human imm
7	15	100.0	672	AAK63395	AAK63395 Human imm
8	15	100.0	877	AD162798	AD162798 Human ova
9	15	100.0	1845	AAAC45833	AAAC45833 Arabidops
10	15	100.0	1939	ABX70923	ABX70923 Novel hum
11	15	100.0	1945	AAAC44652	AAAC44652 Arabidops
12	15	100.0	3972	ABZ14299	ABZ14299 Arabidops
13	15	100.0	11	ACN44506	ACN44506 Human, gen
14	15	93.3	181	AAZ12830	AAZ12830 Human sec
15	15	93.3	300	AAZ12424	AAZ12424 Human gen
16	15	93.3	340	AAZ98669	AAZ98669 Human can
17	15	93.3	314	AAZ75535	AAZ75535 DNA encod
18	15	93.3	341	AAZ67219	AAZ67219 Novel hum
19	15	93.3	372	ACD95670	ACD95670 Human col
20	15	93.3	381	AAZ67260	AAZ67260 Novel hum

ALIGNMENTS

RESULT 1	AAA07571 standard; DNA, 15 BP.
ID	AAA07571;
AC	AAA07571;
DT	29-AUG-2000 (first entry)
XX	
DE	Detoxified Shiga toxin 2 modified segment #4.
XX	
KW	Expression cassette; plasmid maintenance system; Neisseria meningitidis;
KW	post-segregational killing function; ompC promoter; immune response;
KW	vaccine; Salmonella typhi; hepatitis; Haemophilus influenzae type b;
KW	acellular pertussis; varicella; rotavirus; Streptococcus pneumoniae;
KW	cancer vaccine; autoimmune disorder; immunological disease; allergy;
KW	myasthenia gravis; lupus erythematosus; rheumatoid arthritis; therapy;
KW	multiple sclerosis; asthma; ss.
XX	
OS	Salmonella typhi.
XX	
PN	W0200032047-A1.
XX	
PD	08-JUN-2000.
XX	
PF	02-DEC-1999; 99WC-US028499.
XX	
PR	02-DEC-1998; 98US-00204117.
PR	12-OCT-1999; 99US-0158738P.
XX	
PA	(UYMA-) UNIV MARYLAND BALTIMORE.
XX	
PI	Galen JE;
XX	
DR	WPI; 2000-412091/35.
XX	
PT	Expression cassette used as live vector vaccine comprises nucleotide
PT	sequence encoding origin of replication and plasmid maintenance system
PT	which includes a post-segregational killing and a partitioning function.
XX	
PS	Claim 32; Page 92; 127pp; English.
XX	
CC	This sequence is a modified Shiga 2 toxin fragment and can be used in the
CC	expression cassette of the invention. The cassette is an independently

21	14	93.3	384	6	ABN76896	ABN76896 Human ORF
22	14	93.3	431	8	ABX62031	ABX62031 Arabidops
23	14	93.3	466	6	ABL93530	ABL93530 Arabidops
24	14	93.3	483	9	ACH18421	ACH18421 Human adu
25	14	93.3	610	5	ADL36458	ADL36458 Human ova
26	14	93.3	610	5	ADL71298	ADL71298 Human ova
27	14	93.3	612	8	ACA39967	ACA39967 Prokaryot
28	14	93.3	618	3	ACA10902	ACA10902 Human sec
29	14	93.3	623	5	AAH58846	AAH58846 Human SCN
30	14	93.3	737	2	AAZ98728	AAZ98728 Human val
31	14	93.3	744	8	ACA53032	ACA53032 Prokaryot
32	14	93.3	745	3	AAAC10881	AAAC10881 Human sec
33	14	93.3	777	5	AAZ75537	AAZ75537 DNA encod
34	14	93.3	834	4	ABA89060	ABA89060 Escherich
35	14	93.3	960	10	ADH85067	ADH85067 Enterococ
36	14	93.3	1225	6	ABK35807	ABK35807 cDNA sequ
37	14	93.3	1336	6	ABQ54665	ABQ54665 Human ova
38	14	93.3	1357	10	ADC64340	ADC64340 HYPV codi
39	14	93.3	1421	4	AAQ02046	AAQ02046 DNA encod
40	14	93.3	1448	2	AAQ40202	AAQ40202 Sequence
41	14	93.3	1457	13	ADS50509	ADS50509 Bacterial
42	14	93.3	1465	4	AAI60558	AAI60558 Human pol
43	14	93.3	1467	4	AAI58772	AAI58772 Human pol
44	14	93.3	1467	5	ADQ98992	ADQ98992 DNA encod
45	14	93.3	1467	9	ADB48752	ADB48752 Novel hum

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 11:14:05 / Search time 83.643 Seconds
(without alignments)
8689.645 Million cell updates/sec

Title: US-10-750-965-39

Perfect score: 15

Sequence: 1 gaattcgaccact 15

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

GenEmbl:.*
1: gb Da:.*
2: gb Htg:.*
3: gb In:.*
4: gb Om:.*
5: gb OV:.*
6: gb Pac:.*
7: gb Ph:.*
8: gb Pl:.*
9: gb Pr:.*
10: gb Ro:.*
11: gb Ste:.*
12: gb Sy:.*
13: gb Un:.*
14: gb Vi:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	1924	9 AKI29669	AKI29669 Homo sapi
2	15	100.0	3137	8 NCR243517	AJ243517 Neurospor
3	15	100.0	3566	9 EX119906	EX119906 Human DNA
4	15	100.0	17966	2 AC138145	AC138145 Homo sapi
5	15	100.0	190107	9 AC100832	AC100832 Homo sapi
6	15	100.0	349841	1 BX572606	BX572606 Rhodosphe
7	15	93.3	385	6 CO472848	CO472848 Sequence
8	14	93.3	396	6 CO478754	CO478754 Sequence
9	14	93.3	417	6 CO465586	CO465586 Sequence
10	14	93.3	428	6 CO482017	CO482017 Sequence
11	14	93.3	430	6 CO503156	CO503156 Sequence
12	14	93.3	438	6 CO499551	CO499551 Sequence
13	14	93.3	438	6 CO508919	CO508919 Sequence
14	14	93.3	438	6 CO512005	CO512005 Sequence
15	14	93.3	459	6 CO692166	CO692166 Sequence
16	14	93.3	559	6 BD152296	BD152296 Primer fo
17	14	93.3	559	6 AX872234	AX872234 Sequence
18	14	93.3	594	6 CO489052	CO489052 Sequence
19	14	93.3	594	6 CO491123	CO491123 Sequence

c 20	14	93.3	594	6	CO494900	CO494900 Sequence
c 21	14	93.3	966	13	CO496987	CO496987 Sequence
c 22	14	93.3	966	13	AY487538	AY487538 Unculture
c 23	14	93.3	1200	6	AR376947	AR376947 Sequence
c 24	14	93.3	1521	1	AF411070	AF411070 Sphingomo
c 25	14	93.3	1681	9	AK000455	AK000455 Homo sapi
c 26	14	93.3	2133	6	BD159467	BD159467 Primer fo
c 27	14	93.3	2133	6	AX882028	AX882028 Sequence
c 28	14	93.3	2133	6	AK027380	AK027380 Homo sapi
c 29	14	93.3	3075	1	AF127079	AF127079 Salimone11
c 30	14	93.3	7119	3	AF329639	AF329639 Drosophill
c 31	14	93.3	21470	1	AB008733	AB008733 Salimone11
c 32	14	93.3	43596	9	AC091886	AC091886 Homo sapi
c 33	14	93.3	56883	2	AL365182	AL365182 Homo sapi
c 34	14	93.3	60752	2	AC105060	AC105060 Mus muscu
c 35	14	93.3	119184	1	D90909	D90909 Synchocyst
c 36	14	93.3	119638	9	AC024575	AC024575 Homo sapi
c 37	14	93.3	132492	9	AC007616	AC007616 Homo sapi
c 38	14	93.3	142645	9	AC008481	AC008481 Homo sapi
c 39	14	93.3	144000	9	AC007621	AC007621 Homo sapi
c 40	14	93.3	144771	2	AC018610	AC018610 Homo sapi
c 41	14	93.3	152081	9	AC007381	AC007381 Homo sapi
c 42	14	93.3	163049	9	BS000182	BS000182 Pan trogl
c 43	14	93.3	163384	9	AC009180	AC009180 Homo sapi
c 44	14	93.3	164008	2	AC024064	AC024064 Homo sapi
c 45	14	93.3	169250	9	AP002812	AP002812 Homo sapi

ALIGNMENTS

RESULT 1
AKI29669
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S.,

Funakuma, Y., Fujimori, Y., Komiyama, M., Suzuki, Y., Hata, H.,
Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T.,
Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A.,
Kawakami, B., Nagai, K., Isegai, T. and Sugano, S.

COMMENT:
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

FEATURES

COMMENT:
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

FEATURES
source
1. 1924
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ADG01579"
/issue_type="adrenal gland"
/clone_lib="ADG"

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 11:14:05 / Search time 6674.71 Seconds
(without alignments)
8689.645 Million cell updates/sec

Title: US-10-750-965-2

Perfect score: 1197

Sequence: 1 ctcaaatatgagctagcc.....gacgcagcgcgagagcgag 1197

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: GenBank:
1: gb_ha:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1197	100.0	1197	6 AR483258	AR483258 Sequence
2	817.4	68.3	4196	6 AR483257	AR483257 Sequence
3	718.2	60.0	6271	6 AX18406	AX18406 Sequence
4	718.2	60.0	8908	6 AX18423	AX18423 Sequence
5	627.4	52.4	1026	1 ECP15A	ECP15A
6	627.4	52.4	2314	1 AF432497	AF432497
7	627.4	52.4	2553	12 CVE289102	CVE289102
8	627.4	52.4	2568	12 CVE277764	CVE277764
9	627.4	52.4	3210	12 AF361440	AF361440
10	627.4	52.4	3465	6 AX000478	AX000478 Sequence
11	627.4	52.4	3465	6 BD073379	BD073379 Sequence
12	627.4	52.4	3481	6 AX000480	AX000480 Sequence
13	627.4	52.4	3481	6 BD073380	BD073380 Sequence
14	627.4	52.4	3666	12 U66309	U66309
15	627.4	52.4	3720	6 BD136661	BD136661
16	627.4	52.4	3720	6 AX018968	AX018968 Sequence
17	627.4	52.4	3794	6 BD136662	BD136662
18	627.4	52.4	3794	6 AX000474	AX000474 Sequence
19	627.4	52.4	3794	6 AX018970	AX018970 Sequence

20	627.4	52.4	3794	6 BD073377	BD073377
21	627.4	52.4	3801	6 AR493833	AR493833 Sequence
22	627.4	52.4	3810	6 AX000476	AX000476 Sequence
23	627.4	52.4	3810	6 BD073378	BD073378 Sequence
24	627.4	52.4	4245	6 AR069365	AR069365 Sequence
25	627.4	52.4	4245	12 PACYCI84	PACYCI84
26	627.4	52.4	4411	6 AR069366	AR069366 Sequence
27	627.4	52.4	4753	12 AP129432	AP129432
28	627.4	52.4	4975	6 BD136663	BD136663
29	627.4	52.4	4975	6 AX018972	AX018972 Sequence
30	627.4	52.4	5077	6 AX799953	AX799953 Sequence
31	627.4	52.4	5201	6 AR493834	AR493834 Sequence
32	627.4	52.4	5201	6 AR493835	AR493835 Sequence
33	627.4	52.4	5635	12 CV047103	CV047103
34	627.4	52.4	6101	12 SIN417488	SIN417488
35	627.4	52.4	6123	12 SIN417449	SIN417449
36	627.4	52.4	6363	6 AR069367	AR069367
37	627.4	52.4	6758	12 AP121784	AP121784
38	627.4	52.4	7151	12 AY042185	AY042185
39	627.4	52.4	8774	12 IVU69267	IVU69267
40	627.4	52.4	9065	12 AF405698	AF405698
41	627.4	52.4	12168	12 AF405696	AF405696
42	627.4	52.4	12248	12 AF405697	AF405697
43	627.4	52.4	14828	12 AY230218	AY230218
44	627.4	52.4	18658	12 XJ073849	XJ073849
45	626.2	52.3	4523	12 EVE243540	EVE243540

ALIGNMENTS

RESULT 1
AR483258 1197 bp DNA linear PAT 14-MAY-2004
LOCUS AR483258
DEFINITION Sequence 2 from patent US 6703233.
ACCESSION AR483258
VERSION AR483258.1 GI:47245789
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1197)
AUTHORS Galen J.E.
TITLE Plasmid maintenance system for antigen delivery
JOURNAL Patent: US 6703233-A 2 09-MAR-2004;
FEATURES
source 1. 1197
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 1197; DB 6; Length 1197;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTACAAATATGAGCTAGCCCGCTTAATGAGCGGCTTTTCTCGGCTTAGAGATA 60
DB 1 CTACAAATATGAGCTAGCCCGCTTAATGAGCGGCTTTTCTCGGCTTAGAGATA 60
QY 61 CTTAAACGAGGAGTGAAGGCGCGGGAAGCCGTTTTCATAGGCTCGGCCCTG 120
DB 61 CTTAAACGAGGAGTGAAGGCGCGGGAAGCCGTTTTCATAGGCTCGGCCCTG 120
QY 61 CTTAAACGAGGAGTGAAGGCGCGGGAAGCCGTTTTCATAGGCTCGGCCCTG 120
DB 61 CTTAAACGAGGAGTGAAGGCGCGGGAAGCCGTTTTCATAGGCTCGGCCCTG 120
QY 121 ACAAGCATTCAGAAATCGAGCTCAATCACTGTCGCAACCCAGAGACTATATA 180
DB 121 ACAAGCATTCAGAAATCGAGCTCAATCACTGTCGCAACCCAGAGACTATATA 180
QY 181 GATACACAGGCGTTTCCCTGCGGCTCCCTGCTGCTCTGCTGCTCTTTCGGT 240
DB 181 GATACACAGGCGTTTCCCTGCGGCTCCCTGCTGCTCTGCTGCTCTTTCGGT 240
QY 241 TTACCGGTGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 TTACCGGTGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 18:04:09 ; Search time 69.3063 Seconds
(without alignments)
10487.183 Million cell updates/sec

Title: US-10-750-976-37

Perfect score: 15

Sequence: 1 acagcagacgcgtta 15

Scoring table: IDENTITY NUC

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Searched: 4708233 seqs, 24227607955 residues

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Maximum Match 100%

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Database:

GenEmbl:
1: gb_ba:*
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3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_rtc:*
12: gb_ey:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	3959	14	AY547458	AY547458 Avian ort
2	100.0	211113	2	CR391962	CR391962 Dario rer
3	93.3	714	9	HS437219	HS437219 Homo sapi
4	93.3	3312	3	AY433803	AY433803 Trypanoso
5	93.3	5069	5	AF038560	AF038560 Gallus ga
6	93.3	10221	1	AE014558	AE014558 Brucella
7	93.3	10495	1	AE009700	AE009700 Brucella
8	93.3	24523	1	AE008756	AE008756 Salmone
9	93.3	36748	7	AY539836	AY539836 Burkholde
10	93.3	39949	3	AC008782	AC008782 Leishman
11	93.3	106256	2	AC108135	AC108135 Leishman
12	93.3	110000	2	AP006498	AP006498 Continuat
13	93.3	133713	3	AC087838	AC087838 Leishman
14	93.3	147226	9	AC103736	AC103736 Homo sapi
15	93.3	152770	9	AC013602	AC013602 Homo sapi
16	93.3	173839	9	AC026005	AC026005 Homo sapi
17	93.3	181087	2	AC118205	AC118205 Mus muscu
18	93.3	217285	2	AC126317	AC126317 Rattus no
19	93.3	233050	1	AL627271	AL627271 Salmone

C 20	14	93.3	260760	2	AC127861	AC127861 Rattus no
C 21	14	93.3	295050	1	AL591982	AL591982 Listeria
C 22	14	93.3	300523	1	AE016838	AE016838 Salmone
C 23	14	93.3	305325	1	AE016765	AE016765 Escherich
C 24	14	93.3	311600	1	AE016871	AE016871 Pseudomon
C 25	14	93.3	340750	1	BX294135	BX294135 Pirellula
C 26	14	93.3	349980	6	AX641671	AX641671 Sequence
C 27	13.4	89.3	155	8	HV19R	284539 H. vulgare B
C 28	13.4	89.3	227	8	HVE13231R	284559 H. vulgare B
C 29	13.4	89.3	221	8	HVE1325TR	284564 H. vulgare B
C 30	13.4	89.3	232	8	HVE1324VR	284560 H. vulgare B
C 31	13.4	89.3	243	6	AR321328	AR321328 Sequence
C 32	13.4	89.3	318	6	AX048488	AX048488 Sequence
C 33	13.4	89.3	318	6	AX048489	AX048489 Sequence
C 34	13.4	89.3	356	8	HVE08492R	284554 H. vulgare B
C 35	13.4	89.3	413	6	CO481384	CO481384 Sequence
C 36	13.4	89.3	640	14	AF322856	AF322856 Caprine a
C 37	13.4	89.3	798	8	AR388811	AR388811 Sequence
C 38	13.4	89.3	817	8	PSU58023	US8023 Pseudorogn
C 39	13.4	89.3	858	11	CNS0643B	AL401085 T7 end of
C 40	13.4	89.3	1074	6	AR386605	AR386605 Sequence
C 41	13.4	89.3	1104	8	AB189674	AB189674 Philodend
C 42	13.4	89.3	1238	1	AB174823	AB174823 Cellulomo
C 43	13.4	89.3	1281	9	BC064028	BC064028 Homo sapi
C 44	13.4	89.3	1404	3	AF026516	AF026516 Fungiculin
C 45	13.4	89.3	1539	6	AX568254	AX568254 Sequence

ALIGNMENTS

RESULT 1	AY547458	3959 bp	RNA	linear	VRL 04-AUG-2004
LOCUS	AY547458				
DEFINITION	Avian orthoreovirus inner capsid protein lambda-A gene, complete cds.				
ACCESSION	AY547458				
VERSION	AY547458.1	GI:47420812			
KEYWORDS					
SOURCE	Avian orthoreovirus				
ORGANISM	Avian orthoreovirus				
REFERENCE	Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.				
AUTHORS	1. (bases 1 to 3959) Touris-Otero, F., Cortez-San Martin, M., Martinez-Costas, J. and Benavente, J.				
TITLE	Avian Reovirus Morphogenesis Occurs Within Viral Factories and Begins with the Selective Recruitment of sigma3 and lambda3 to mRN3 Inclusions				
JOURNAL	J. Mol. Biol. 341 (2), 361-374 (2004)				
PUBMED	15276829				
REFERENCE	2. (bases 1 to 3959) Cortez-San Martin, M., Touris-Otero, F., Martinez-Costas, J. and Benavente, J.				
AUTHORS	Direct Subassembly				
TITLE	Submitted (13-FEB-2004) Biología, Universidad de Santiago de Compostela, Facultad de Farmacia Campus Sur s/n, Santiago de Compostela, La Coruña 15782, Spain				
JOURNAL	Compostela				
PUBMED	1..3959				
REFERENCE	Location/Qualifiers				
AUTHORS	1..3959				
TITLE	/organism="Avian orthoreovirus"				
JOURNAL	/mol_type="genomic RNA"				
PUBMED	/strain="S1133"				
REFERENCE	/db_xref="taxon:38170"				
AUTHORS	/segment="L1"				
TITLE	/country="USA"				
JOURNAL	22..3903				
PUBMED	/codon_start=1				
REFERENCE	/product="inner capsid protein lambda-A"				
AUTHORS	/protein_id="A4720813.1"				
TITLE	/db_xref="GI:47420813"				
JOURNAL	/translation="MSRRVARRRRHDAESKDTKDTNKSPPESIDAKSTDSATDKK				
PUBMED	VTAPPPNNNASTPSTDGASQTSVAKQTHNDASVESAIPRTVSSDGDGDGMGAVK				
REFERENCE	SODAPYAAVVDNNKRDVVEGGAGSDKNAITKTVSGVDVNDGAVKVPAPAKATISSAQA				

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 18:04:09 ; Search time 157.094 Seconds
(without alignments)
10487.183 Million cell updates/sec

Title: US-10-750-976-36

Perfect score: 34
Sequence: 1 agatcmtaancatccacagagagatctgatg, 34

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_da: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pac: *
7: gb_pl: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	76.5	4196	6	AR483257 Sequence
2	22.2	65.3	349	6	CO477694 Sequence
3	22.2	65.3	400	6	CO498897 Sequence
4	22.2	65.3	400	6	CO507866 Sequence
5	22.2	64.7	229957	10	AL670231 Sequence
6	21.6	63.5	639	11	BV073720 Sequence
7	21.6	63.5	191804	2	CR385041 Sequence
8	21.6	63.5	199321	2	AC141872 Sequence
9	21.6	62.9	319737	2	AC126267 Sequence
10	21.4	62.9	246739	2	AC133052 Sequence
11	21.2	62.4	32	6	AL8778 Sequence
12	21.2	62.4	102	6	AL8333 Sequence
13	21.2	62.4	161	6	IL3979 Sequence
14	21.2	62.4	3712	6	AA9987 Sequence
15	21.2	62.4	3754	6	A37074 Sequence
16	21.2	62.4	3754	6	A42478 Sequence
17	21.2	62.4	3754	6	AR257551 Sequence
18	21.2	62.4	3754	6	AR257551 Sequence
19	21.2	62.4	3754	6	AR453380 Sequence

20	21.2	62.4	3769	6	A37075 Sequence 18
21	21.2	62.4	3769	6	A49988 Sequence 5
22	21.2	62.4	3769	6	AR453381 Sequence
23	21.2	62.4	4366	6	AR2484 Sequence 12
24	21.2	62.4	4366	6	AR257557 Sequence
25	21.2	62.4	4378	6	AR257554 Sequence 9
26	21.2	62.4	4378	6	AR257554 Sequence
27	21.2	62.4	4378	6	AR257554 Sequence
28	21.2	62.4	4378	6	AR257554 Sequence
29	21.2	62.4	4378	6	AR257554 Sequence
30	21.2	62.4	4378	6	AR257554 Sequence
31	21.2	62.4	4378	6	AR257554 Sequence
32	21.2	62.4	4378	6	AR257554 Sequence
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ALIGNMENTS

RESULT 1	AR483257	4196 bp	DNA	linear	PAT 14-MAY-2004
LOCUS	AR483257				
DEFINITION	Sequence 1 from patent US 6703233.				
ACCESSION	AR483257				
VERSION	AR483257.1	GI:47245788			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 4196)				
AUTHORS	Galen, J.R.				
TITLE	Plasmid maintenance system for antigen delivery				
JOURNAL	Patent: US 6703233-A1 09-MAR-2004;				
FEATURES	Location/Qualifiers				
source	1..4196				
ORIGIN	/organism="unknown"				
	/mol_type="genomic DNA"				

Query Match	76.5%	Score 26;	DB 6;	Length 4196;
Best Local Similarity	96.3%	Pred. No. 0.16;		
Matches	26;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0;
Db	470	TAACATCCACAGAGATCTGATG	496	
8	TAACATCCACAGAGATCTGATG	34		
RESULT 2	CO477694	349 bp	DNA	linear
LOCUS	CO477694			
DEFINITION	Sequence 9561 from Patent WO0160860.			
ACCESSION	CO477694			
VERSION	CO477694.1	GI:41443313		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Butcheria; Primates; Catarrhini; Hominiidae; Homo.			
	Schlegel, R., Bredge, W.O. and Monahan, J.R.			

